

# EXHIBIT 4

DR EMBL; AE004969; AAW90230.1; -; Genomic\_DNA.  
DR RefSeq; YP\_208642.1; -.  
DR HSSP; P15770; 1NYT.  
DR STRING; Q5F6F7; -.  
DR GeneID; 3281609; -.  
DR GenomeReviews; AE004969\_GR; NGO1602.  
DR KEGG; ngo:NGO1602; -.  
DR NMPDR; fig|242231.4.peg.1691; -.  
DR HOGENOM; HBG553408; -.  
DR OMA; DLYCVMG; -.  
DR BioCyc; NGON242231:NGO1602-MON; -.  
DR GO; GO:0005737; C:cytoplasm; IEA:InterPro.  
DR GO; GO:0050661; F:NADP or NADPH binding; IEA:InterPro.  
DR GO; GO:0004764; F:shikimate 5-dehydrogenase activity; IEA:HAMAP.  
DR GO; GO:0009073; P:aromatic amino acid family biosynthetic pro...;  
IEA:HAMAP.  
DR GO; GO:0055114; P:oxidation reduction; IEA:UniProtKB-KW.  
DR HAMAP; MF\_00222; -; 1.  
DR InterPro; IPR016040; NAD(P)-bd\_dom.  
DR InterPro; IPR011342; Quinate/shikimate\_5-DH.  
DR InterPro; IPR013708; Shikimate\_DH-bd\_N.  
DR InterPro; IPR006151; Shikm\_DH/Glu-tRNA\_Rdtase.  
DR Gene3D; G3DSA:3.40.50.720; NAD(P)-bd; 1.  
DR Pfam; PF01488; Shikimate\_DH; 1.  
DR Pfam; PF08501; Shikimate\_dh\_N; 1.  
PE 3: Inferred from homology;  
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;  
KW Complete proteome; NADP; Oxidoreductase.  
FT CHAIN 1 269 Shikimate dehydrogenase.  
FT /FTid=PRO\_1000021311.  
FT NP\_BIND 130 134 NADP (By similarity).  
FT ACT\_SITE 68 68 Proton acceptor (Potential).  
SQ SEQUENCE 269 AA; 28649 MW; 07FFD1FCF1A5FDD9 CRC64;  
MHALPRYAVF GNPAASHKSP QIHQQFALQE GVDIEYGRIC ADIGGFAQAV STFFETGGCC  
ANVTVPFKQE AFHLADEHSD RALAAGAVNT LVWLEDGRIR GDNTDGIGLA NDIQVKNIA  
IEGKTILLLG AGGAVRGVIP VLKEHRPARI VIANRTRAKA EELARLFGEI AVPMADVNGG  
FDIIINGTSG GLSGQLPAVS PKIFRDCRLA YDMVYGEAAK PFLDFARQSG AKKTDAGLGM  
LVGQAAASYA LWRGFKPDIR PVIEHMKAL

DR EMBL; AE004969; AAW90292.1; -; Genomic\_DNA.  
DR RefSeq; YP\_208704.1; -.  
DR STRING; Q5F695; -.  
DR GeneID; 3281268; -.  
DR GenomeReviews; AE004969\_GR; NGO1667.  
DR KEGG; ngo:NGO1667; -.  
DR NMPDR; fig|242231.4.peg.1808; -.  
DR HOGENOM; HBG704071; -.  
DR OMA; MVDTWVT; -.  
DR BioCyc; NGON242231:NGO1667-MON; -.  
DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.  
DR GO; GO:0008666; F:2,3,4,5-tetrahydropyridine-2,6-dicarboxylat...;  
IEA:HAMAP.

DR GO; GO:0019877; P:diaminopimelate biosynthetic process; IEA:HAMAP.  
 DR HAMAP; MF\_00811; -; 1.  
 DR InterPro; IPR005664; DapD.  
 DR InterPro; IPR001451; Hexapep\_transf.  
 DR InterPro; IPR018357; Hexapep\_transf\_CS.  
 DR InterPro; IPR011004; Trimer\_LpxA-like.  
 DR Pfam; PF00132; Hexapep; 4.  
 DR PROSITE; PS00101; HEXAPEP\_TRANSFERASES; 1.  
 PE 3: Inferred from homology;  
 KW Acyltransferase; Amino-acid biosynthesis; Complete proteome;  
 KW Cytoplasm; Diaminopimelate biosynthesis; Lysine biosynthesis;  
 Repeat;  
 KW Transferase.  
 FT CHAIN 1 273 2,3,4,5-tetrahydropyridine-2,6-  
 FT dicarboxylate N-succinyltransferase.  
 FT /FTid=PRO\_0000196950.  
 FT BINDING 104 104 Substrate (By similarity).  
 FT BINDING 141 141 Substrate (By similarity).  
 SQ SEQUENCE 273 AA; 29305 MW; 762DD5A632781146 CRC64;  
 MSLNQIIETA FENRADITPT TVAPEVKEAV LETIRQLDSG KLRVAERLGV GEWKVNEWAK  
 KAVLLSFRIQ DNEVLNDGVN KYFDKVP TKF ADWSEDEFKN AGFRAVPGAV ARRGSFVAKN  
 AVLMPGYVNI GAYVDEGAMV DTWATVGS CA QIGKNVHLSG GVGIGGVLEP LQAAPTIID  
 NCFIGARSEI VEGAIVEEGS VISMGVFIGQ STKIFDRITG EIYQGRVPAG SVVVSGLPS  
 KDGSHSLYCA VIVKRVDATQ RAKTSVNELL RGI

DR EMBL; AE004969; AAW89131.1; -; Genomic\_DNA.  
 DR RefSeq; YP\_207543.1; -.  
 DR PDB; 3D1T; X-ray; 2.20 A; A/B=1-257.  
 DR PDB; 3D20; X-ray; 2.04 A; A/B=1-257.  
 DR PDBsum; 3D1T; -.  
 DR PDBsum; 3D20; -.  
 DR STRING; Q5F9K6; -.  
 DR GeneID; 3282560; -.  
 DR GenomeReviews; AE004969\_GR; NGO0387.  
 DR KEGG; ngo:NGO0387; -.  
 DR NMPDR; fig|242231.4.peg.732; -.  
 DR HOGENOM; HBG626871; -.  
 DR OMA; SLMDYEV; -.  
 DR BioCyc; NGON242231:NGO0387-MON; -.  
 DR GO; GO:0003934; F:GTP cyclohydrolase I activity; IEA:EC.  
 DR HAMAP; MF\_01527; -; 1.  
 DR InterPro; IPR003801; DUF198.  
 DR Pfam; PF02649; DUF198; 1.  
 PE 1: Evidence at protein level;  
 KW 3D-structure; Complete proteome; Hydrolase.  
 FT CHAIN 1 257 GTP cyclohydrolase folE2.  
 FT /FTid=PRO\_0000147714.  
 FT SITE 147 147 May be catalytically important (By  
 FT similarity).  
 FT STRAND 18 21  
 FT STRAND 26 32  
 FT STRAND 39 47  
 FT STRAND 49 51  
 FT HELIX 61 69  
 FT HELIX 76 89  
 FT STRAND 97 108

FT STRAND 115 125  
 FT STRAND 136 146  
 FT HELIX 148 153  
 FT STRAND 160 173  
 FT HELIX 178 185  
 FT STRAND 188 191  
 FT HELIX 198 210  
 FT HELIX 215 228  
 FT STRAND 232 241  
 FT STRAND 246 256  
 SQ SEQUENCE 257 AA; 28747 MW; A0235399C3EDF2A9 CRC64;  
 MNAIADVQSS RDLRNLPINQ VGIKDLRFPI TLKTAEGTQS TVARLTMITVY LPAEQKGTHM  
 SRFVALMEQH TEVLDFSQLH RLTAEMVALL DSRAGKISVS PFFFRKKTAP VSGIRSLDDY  
 DVSLTGEMKD GAYGHSMKVM IPVTSLCPCS KEISQYGAHN QRSHVTVSLT SDAEVGIEEV  
 IDYVETQASC QLYGLLKRPD EKYVTEKAYE NPKFVEDMVR DVATSLIADK RIKSFVVESE  
 NFESIHNHSA YAYIAYP  
  
 DR EMBL; AE004969; AAW90424.1; -; Genomic\_DNA.  
 DR RefSeq; YP\_208836.1; -.  
 DR HSSP; POA722; 1LXA.  
 DR STRING; Q5F5W3; -.  
 DR GeneID; 3282363; -.  
 DR GenomeReviews; AE004969\_GR; NGO1806.  
 DR KEGG; ngo:NGO1806; -.  
 DR NMPDR; fig|242231.4.peg.1389; -.  
 DR HOGENOM; HBG659295; -.  
 DR OMA; GHTSIGE; -.  
 DR BioCyc; NGON242231:NGO1806-MON; -.  
 DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.  
 DR GO; GO:0008780; F:acyl-[acyl-carrier-protein]-UDP-N-acetylglu...;  
 IEA:HAMAP.  
 DR GO; GO:0009245; P:lipid A biosynthetic process; IEA:HAMAP.  
 DR HAMAP; MF\_00387; -; 1.  
 DR InterPro; IPR001451; Hexapep\_transf.  
 DR InterPro; IPR010137; Lipid\_A\_lpxA.  
 DR InterPro; IPR011004; Trimer\_LpxA-like.  
 DR Pfam; PF00132; Hexapep; 6.  
 DR PIRSF; PIRSF000456; UDP-GlcNAc\_acltr; 1.  
 DR PROSITE; PS00101; HEXAPEP\_TRANSFERASES; FALSE\_NEG.  
 PE 3: Inferred from homology;  
 KW Acyltransferase; Complete proteome; Cytoplasm; Lipid A  
 biosynthesis;  
 KW Lipid synthesis; Repeat; Transferase.  
 FT CHAIN 1 258 Acyl-[acyl-carrier-protein]--UDP-N-  
 FT acetylglucosamine O-acetyltransferase.  
 FT /FTid=PRO\_0000302582.  
 SQ SEQUENCE 258 AA; 28171 MW; B8B5D9D2EE8CCDD3 CRC64;  
 MTLIHPTAVI DPKAELD SGV KVGAYTVIGP NVIRIGANTEI GPHAVINGHT TIGENNRIFQ  
 FASLGEIPQD KKYRDEPTKL IIGNGNTIRE FTTFNLGTVT GIGETRIGDD NWIMAYCHLA  
 HDCVVGNIHTI FANNASLAGH VTGVDYVVLG GYTLVFQFCR IGDYAMTAFAGVHKDVPY  
 FMASGYRAEP AGLNSEGMRR NGFTAQISA VKDVYKTYLH RGIPFEEAKA DILRRAETQA  
 ELAVFQDDFA QSTRGIIR

DR EMBL; AE004969; AAW90138.1; -; Genomic\_DNA.  
 DR RefSeq; YP\_208550.1; -.

DR HSSP; P94556; 1ZUW.  
 DR STRING; Q5F6P9; -.  
 DR GeneID; 3281584; -.  
 DR GenomeReviews; AE004969\_GR; NGO1500.  
 DR KEGG; ngo:NGO1500; -.  
 DR NMPDR; fig|242231.4.peg.1517; -.  
 DR HOGENOM; HBG645102; -.  
 DR OMA; NSPPREV; -.  
 DR BioCyc; NGON242231:NGO1500-MON; -.  
 DR GO; GO:0008881; F:glutamate racemase activity; IEA:HAMAP.  
 DR GO; GO:0007047; P:cell wall organization; IEA:UniProtKB-KW.  
 DR GO; GO:0009252; P:peptidoglycan biosynthetic process; IEA:HAMAP.  
 DR GO; GO:0008360; P:regulation of cell shape; IEA:UniProtKB-KW.  
 DR HAMAP; MF\_00258; -. 1.  
 DR InterPro; IPR015942; Asp/Glu/hydantoin\_racemase.  
 DR InterPro; IPR001920; Asp/Glu\_race.  
 DR InterPro; IPR018187; Asp/Glu\_racemase\_AS.  
 DR InterPro; IPR004391; Glu\_race.  
 DR Gene3D; G3DSA:3.40.50.1860; Asp/Glu\_race; 1.  
 DR Pfam; PF01177; Asp\_Glu\_race; 1.  
 DR PROSITE; PS00923; ASP\_GLU\_RACEMASE\_1; FALSE\_NEG.  
 DR PROSITE; PS00924; ASP\_GLU\_RACEMASE\_2; 1.  
 PE 3: Inferred from homology;  
 KW Cell shape; Cell wall biogenesis/degradation; Complete proteome;  
 KW Isomerase; Peptidoglycan synthesis.  
 FT CHAIN 1 270 Glutamate racemase.  
 FT /FTID=PRO\_1000047589.  
 SQ SEQUENCE 270 AA; 29515 MW; 913E8ABBA2805564 CRC64;  
 MENIGRQRPI GVFDGIGGL TNVRALMERL PMENIIYFGD TARVPYGTKS KATIENFSMQ  
 IVDFLLGHDV KAMVIACNTI AAVAGRKRIR KTGNNMPVLVD ISAGAKAALA TTRNNKIGII  
 ATNTTVNSNA YARAIHRDNP DTLVRTQAAP LLVPLVEEGW LEHEVTRLTV CEYLKPLLD  
 GIDTLVLGCT HFPLLKPLIG REAHNVALVD SAITTAEEA RVLAQEGLLD TGNNNPDYRF  
 YVSDIPLKFR TIGERFLGRT MEQIEMVSLG

DR EMBL; AE004969; AAW89865.1; -. Genomic\_DNA.  
 DR RefSeq; YP\_208277.1; -.  
 DR STRING; Q5F7H2; -.  
 DR GeneID; 3281969; -.  
 DR GenomeReviews; AE004969\_GR; NGO1206.  
 DR KEGG; ngo:NGO1206; -.  
 DR NMPDR; fig|242231.4.peg.1064; -.  
 DR HOGENOM; HBG541103; -.  
 DR OMA; IFMSVFN; -.  
 DR BioCyc; NGON242231:NGO1206-MON; -.  
 DR GO; GO:0048037; F:cofactor binding; IEA:InterPro.  
 DR GO; GO:0004609; F:phosphatidylserine decarboxylase activity;  
 IEA:HAMAP.  
 DR GO; GO:0006646; P:phosphatidylethanolamine biosynthetic process;  
 IEA:InterPro.  
 DR HAMAP; MF\_00664; -. 1.  
 DR InterPro; IPR003817; PS\_Dcarbxyase.  
 DR InterPro; IPR004428; PtdSer\_deCO2ase\_related.  
 DR Pfam; PF02666; PS\_Dcarbxyase; 1.  
 PE 3: Inferred from homology;

KW Complete proteome; Decarboxylase; Lyase; Phospholipid biosynthesis;

KW Pyruvate; Zymogen.

FT CHAIN 1 182 Phosphatidylserine decarboxylase beta chain (By similarity).

FT /FTid=PRO\_0000042279.

FT CHAIN 183 259 Phosphatidylserine decarboxylase alpha chain (By similarity).

FT /FTid=PRO\_0000042280.

FT SITE 182 183 Cleavage (non-hydrolytic) (By similarity).

FT MOD\_RES 183 183 Pyruvic acid (Ser) (By similarity).

SQ SEQUENCE 259 AA; 28294 MW; A4D013CF6066A7BE CRC64; MNRLYPHPII AREGWPIIGG GLALSLVSM CCGWWSLPFW VFTVFALQFF RDPAREIPQN PEAVLSPVDG RIVVVERARD PYRDVDALKI SIFMNVFNH SOKSPADCTV TKVVYNKGKF VNADLLKAST ENERNVLAT TASGREITFV QVAGLVARRI LCYTQAGAKL SRGERYGFIR FGSRVDMYLP VDAQAQAIG DKVTGVKTVL ARLPLTDSQA DPVSQAASVE TAANPSAEQQ QIEAAAAIKI AAVQDVLKD

DR EMBL; AE004969; AAW90342.1; -; Genomic\_DNA.

DR RefSeq; YP\_208754.1; -.

DR HSSP; P00909; 1PII.

DR STRING; Q5F645; -.

DR GeneID; 3281235; -.

DR GenomeReviews; AE004969\_GR; NGO1721.

DR KEGG; ngo:NGO1721; -.

DR NMPDR; fig|242231.4.peg.1924; -.

DR HOGENOM; HBG540956; -.

DR OMA; PLLCKDF; -.

DR BioCyc; NGON242231:NGO1721-MON; -.

DR GO; GO:0004425; F:indole-3-glycerol-phosphate synthase activity; IEA:HAMAP.

DR GO; GO:0000162; P:tryptophan biosynthetic process; IEA:HAMAP.

DR HAMAP; MF\_00134; -; 1.

DR InterPro; IPR013785; Aldolase\_TIM.

DR InterPro; IPR013798; Indole-3-glycerol\_P\_synth.

DR InterPro; IPR001468; Indole-3-GPS\_central.

DR InterPro; IPR011060; RibuloseP-bd\_barrel.

DR Gene3D; G3DSA:3.20.20.70; Aldolase\_TIM; 1.

DR Pfam; PF00218; IGPS; 1.

DR PROSITE; PS00614; IGPS; 1.

PE 3; Inferred from homology;

KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;

KW Complete proteome; Decarboxylase; Lyase; Tryptophan biosynthesis.

FT CHAIN 1 260 Indole-3-glycerol phosphate synthase.

FT /FTid=PRO\_1000018508.

SQ SEQUENCE 260 AA; 28622 MW; 097107AE32AD93AB CRC64; MTDILNKILA TKAQEVAAQK AAVNAEHIRA LAEEAAPVRS FIDSIRGKHR LNLPAVIAEI KKASPSKGLI RPDFRPAEIA RAYENAGAAC LSVLTDEPYF QGSPEYLRQA REAVLLPVLR KDFIIDEYQV YQARAWGADA VLLIAAALEQ GQLERFEALA HELGMTVLLE LHDTELEK RNLTPPLWGV NNRNLRTEFV SLDQTLSELL ALEGKTVVTE SGITGKADVE FMRARGVHTF LIGETFMRAD DIGAEVGLKF

DR EMBL; AE004969; AAW90429.1; -; Genomic\_DNA.  
 DR RefSeq; YP\_208841.1; -.  
 DR STRING; Q5F5V8; -.  
 DR GeneID; 3282256; -.  
 DR GenomeReviews; AE004969\_GR; NGO1811.  
 DR KEGG; ngo:NGO1811; -.  
 DR NMPDR; fig|242231.4.peg.1394; -.  
 DR HOGENOM; HBG621020; -.  
 DR OMA; QSKTPFR; -.  
 DR BioCyc; NGON242231:NGO1811-MON; -.  
 DR GO; GO:0009982; F:pseudouridine synthase activity; IEA:HAMAP.  
 DR GO; GO:0003723; F:RNA binding; IEA:InterPro.  
 DR GO; GO:0031119; P:tRNA pseudouridine synthesis; IEA:HAMAP.  
 DR HAMAP; MF\_00171; -; 1.  
 DR InterPro; IPR020103; PsdUridine\_synth\_cat\_dom.  
 DR InterPro; IPR001406; PsdUridine\_synth\_TrUA.  
 DR InterPro; IPR020097; PsdUridine\_synth\_TrUA\_a/b\_dom.  
 DR InterPro; IPR020095; PsdUridine\_synth\_TrUA\_C.  
 DR InterPro; IPR020094; PsdUridine\_synth\_TrUA\_N.  
 DR Gene3D; G3DSA:3.30.70.580; PseudoU\_synth\_1; 1.  
 DR Gene3D; G3DSA:3.30.70.660; PseudoU\_synth\_1; 1.  
 DR PANTHER; PTHR11142; PseudoU\_synth\_1; 1.  
 DR Pfam; PF01416; PseudoU\_synth\_1; 2.  
 DR PIRSF; PIRSF001430; tRNA\_psdUrid\_synth; 1.  
 PE 3: Inferred from homology;  
 KW Complete proteome; Isomerase; tRNA processing.  
 FT CHAIN 1 265 tRNA pseudouridine synthase A.  
 FT /FTid=PRO\_0000057418.  
 FT ACT\_SITE 58 58 Nucleophile (By similarity).  
 SQ SEQUENCE 265 AA; 28806 MW; 4A69B5CE60B97A48 CRC64;  
 MDTAQKQRWA ITLSYDGSRF YGWQKQAGGV PTVQAALETA LARIAGESVA TTVAGRTDTG  
 VHATAQVVHF DTAAVRPAQA WIRGVNAHLP EGI AVLHARQ VAPGFHARFD ASGRHRYLL  
 ESAPVRSPLL KNRAGWTHLE LDIGPMRRAA ALLVGEQDFS SFRAAGCOAK SPVKTIYRAD  
 LTQSAGLVRL DLHGNAFLHH MVRNIMGALV YVSGRSLVE GFAALIQERS RLKAPPTFMP  
 DGLYLTVGDV PGAYGIVRPQ IPEWL

DR EMBL; AE004969; AAW89536.1; -; Genomic\_DNA.  
 DR RefSeq; YP\_207948.1; -.  
 DR STRING; Q5F8F1; -.  
 DR GeneID; 3282206; -.  
 DR GenomeReviews; AE004969\_GR; NGO0826.  
 DR KEGG; ngo:NGO0826; -.  
 DR NMPDR; fig|242231.4.peg.120; -.  
 DR HOGENOM; Q5F8F1; -.  
 DR OMA; MWIDDIY; -.  
 DR PhylomeDB; Q5F8F1; -.  
 DR BioCyc; NGON242231:NGO0826-MON; -.  
 DR InterPro; IPR002110; Ankyrin\_rpt.  
 DR InterPro; IPR020683; Ankyrin\_rpt-contain\_dom.  
 DR InterPro; IPR018756; DUF2314.  
 DR Gene3D; G3DSA:1.25.40.20; ANK; 1.  
 DR Pfam; PF00023; Ank; 1.  
 DR Pfam; PF10077; DUF2314; 1.  
 DR SMART; SM00248; ANK; 1.  
 DR PROSITE; PS50297; ANK\_REP\_REGION; 1.

DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 PE 4: Predicted;  
 KW Complete proteome.  
 SQ SEQUENCE 252 AA; 28937 MW; 5F1A9BEDFADD1740 CRC64;  
 MGDSVIYYVE QADEPVNRAG ERARKTFKYF WRELFWERRR IISALDFAMV KVPFFQDGED  
 GEICEHMMWID DIYFDGLYIY GVLNNEPGGL TNVEQGESVC VPVGDISDWM FVCNGIPYGG  
 FTVQAMRGQM TEEERTEHDT AWGIDFGDPG QVLPVYEEKE HPENLEEHPM CRNCIDDFRQ  
 QLSQNPDFLH EQDEDGYTPL HHEAMAGNAL MVQAMLEYGA NPASKTSEGY TALDFARLTG  
 WQNVADLLEP RH